

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 23, 2003, 21:44:31 ; Search time 215 Seconds

(without alignments)
3659.801 Million cell updates/sec

File: US-09-745-506-37

Perfect score: 350
Sequence: 1 MDKALSLSDPASFASF.....LEKNITLSETRDPLQV 350

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1517243 seqs, 1124081882 residues

Word size: 1

Total number of hits satisfying chosen parameters: 3030518

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	350	100.0	1681	14	US-10-198-846-13222 Sequence 13222, A

2	191	54.6	1614	14	US-10-198-846-12938	Sequence 12938, A
3	90	25.7	828	14	US-10-198-846-6276	Sequence 6276, Ap
4	73	20.9	465	9	US-09-864-761-10530	Sequence 10530, A
5	69	19.7	208	9	US-09-864-761-27152	Sequence 27152, A
6	53	15.1	394	11	US-09-960-352-10848	Sequence 10848, A
7	53	15.1	480	11	US-09-918-995-19746	Sequence 19746, A
8	51	14.6	2922	14	US-10-177-900-10	Sequence 10, Ap1
9	16	4.6	817	13	US-10-027-632-11386	Sequence 161386, A
10	16	4.6	817	13	US-10-027-632-11387	Sequence 161387, A
11	13	3.7	765	13	US-10-027-632-16268	Sequence 16268, A
12	13	2.9	400	8	US-08-781-986A-779	Sequence 779, App
13	8	2.3	333	9	US-08-781-986A-4577	Sequence 4577, Ap
14	8	2.3	383	9	US-09-764-869-65	Sequence 65, Ap1
15	8	2.3	383	14	US-10-091-504-65	Sequence 65, Ap1
16	8	2.3	400	8	US-08-781-986A-3695	Sequence 3695, Ap
17	8	2.3	561	9	US-09-813-242-1909	Sequence 26722, A
18	8	2.3	569	11	US-09-918-995-26722	Sequence 26722, A
19	8	2.3	629	13	US-10-027-632-232135	Sequence 232135, A
20	8	2.3	629	13	US-10-027-632-232136	Sequence 232136, A
21	8	2.3	633	13	US-10-027-632-279793	Sequence 279793, A
22	8	2.3	637	13	US-10-027-632-218904	Sequence 218904, A
23	8	2.3	637	13	US-10-027-632-218905	Sequence 218905, A
24	8	2.3	637	13	US-10-027-632-218906	Sequence 218906, A
25	8	2.3	645	13	US-10-027-632-319486	Sequence 319486, A
26	8	2.3	652	10	US-09-903-814-3	Sequence 3, Ap11
27	8	2.3	725	9	US-09-815-242-4772	Sequence 4772, Ap
28	8	2.3	834	13	US-10-027-632-173418	Sequence 173418, A
29	8	2.3	834	13	US-10-027-632-173419	Sequence 173419, A
30	8	2.3	917	13	US-10-027-632-130225	Sequence 130225, A
31	8	2.3	1069	9	US-09-770-445-136	Sequence 136, App
32	8	2.3	1716	14	US-10-156-761-3688	Sequence 3688, Ap
33	8	2.3	1785	14	US-10-156-761-4784	Sequence 4784, Ap
34	8	2.3	2085	10	US-09-738-626-2027	Sequence 2027, Ap
35	8	2.3	3903	8	US-10-103-311-631	Sequence 631, App
36	8	2.3	3822	12	US-10-311-453-1070	Sequence 1070, Ap
37	8	2.3	9632	10	US-09-764-868-1399	Sequence 1399, Ap
38	8	2.3	9730	10	US-09-764-868-1400	Sequence 1400, Ap
39	8	2.3	11271	9	US-08-781-986A-11	Sequence 11, Ap1
40	8	2.3	16018	8	US-09-764-869-1384	Sequence 1384, Ap
41	8	2.3	16018	14	US-10-091-504-1384	Sequence 1384, Ap
42	8	2.3	17674	9	US-10-311-453-1317	Sequence 1317, Ap
43	8	2.3	22400	12	US-09-764-869-1385	Sequence 1385, Ap
44	8	2.3	22400	14	US-10-091-504-1385	Sequence 1385, Ap
45	8	2.3	32195	10	US-09-764-847-1512	Sequence 1512, Ap

ALIGNMENTS

RESULT 1
US-10-198-846-13222 Application US/10198846
Publication NO. US2003009974A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steilmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198, 846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13222
LENGTH: 1681
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature

LOCATION: 1, 2, 1675, 1676, 1677, 1678, 1679, 1680, 1681
OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13222

Alignment Scores:

Pred. No.:	0	Length:	1681
Score:	350.00	Matches:	350
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-09-745-506-37 (1-350) x US-10-198-846-13222 (1-1681)

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DB 239 ATGATATTGAAGGCTCCCTTCTTCTGTAATGACCTTGACCTCCCTGTTGCGAG 298
QY 21 SerTTrpAspAsnValIglLeuLeuValIglProSerProPheIsthValAsnThrLeu 40
DB 299 AGTTGGACAAATGTTGATTAAGTGTGGACCAAGCCACACACTACTGTAATACACTC 358
QY 41 PheLeuThrAsnAspLeuThrIgluValIgluValIgluValIgluValIgluValIgluVal 60
DB 359 TTCTGACCAATGACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 418
QY 61 LeuLeuSerYrHisProIlePheArgProMetIlyAsnIglIleThrTrpAsnThr 80
DB 419 CTCAATCTCTCTCCACATCCGCTATCTCCGACCCATGAAAGCCATACCTGGAAACCA 478
QY 81 TrpYsGluArgLeuValIleArgAlaLeuGluAsnArgValIglIleYrSerProHis 100
DB 479 TGGAAAGGAGCCCTGGTGTATCCGGGCTGTGGAGAACAGTCCGATATCTCTCTCAT 538
QY 101 ThrAlaYrAspAlaAlaProIleGluValIAsnAsnTrpLeuAlaIlySglYleuGlyAla 120
DB 539 ACAGCCTATGATGCTGGCGCCCGGCGGTCAACAACCTGTTGGCTAAAGGCTTGAGACT 598
QY 121 CysThrSerArgProIleHisProSerIlyAsnAlaProAsnYrProThrGluGlyAsnHis 140
DB 599 TGTACCTCCAGGCGCCATCATCTCCAAAGCTCCCAATCCCTACAGAGGAAACAC 658
QY 141 ArgValIgluPheAsnValAsnYrThrGlnAspLeuAspYsValMetSerAlaValIys 160
DB 659 CGAGTAGAATTCACAGTTAACTACACCAAGACCTGGCAAAAGTCATGTGCACTGAAA 718
QY 161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGlnThr 180
DB 719 GGAATGACGGTGTTCGTCACTCTTTCTGCTAGACTGTAATGAGAGAACAAACA 778
QY 181 ArgIleAsnLeuAsnCysThrGlnIlyAlaLeuMetGlnValIAspPheLeuSerArg 200
DB 779 CGGATTTAATCTGAATTTGTAATCAGAAAGCTTTGATGAGAGTGTGATTTCTTCCCGG 838
QY 201 AsnYsGlnLeuYrGlnIlyThrGluIleLeuSerIleGluYrProLeuLeuLeuHis 220
DB 839 AACAAACACTTTATACAGAAAGAGGAAATTTCTGTACGAGAACCTTTGCTTCTACAT 898
QY 221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
DB 899 ACTGGAATGGAGCGGTATGACACACTGATGATGTCTCCCTGGCAACCATGATGTAT 958
QY 241 ArgIleYrArgHisLeuIlyLeuSerHisIleArgLeuAlaLeuGlyValIglYrThr 260
DB 959 CGAATTAATAAGACCTTAATATCATATTCCTTAAGCCCTTGGGGTGGGAGAAC 1018
QY 261 LeuGluSerGlnValIlyValIAlaLeuCysAlaGlySerGlySerSerValLeuGln 280
DB 1019 TTAAAGTCTCAAGTCAAAAGCTGGCCCTGTGTCTGTGCTGGAGAGCGCTTCTGAG 1078
QY 281 GlyIleValIgluAlaAspLeuYrLeuThrGlyGluMetSerHisHisAspThrLeuAspAla 300
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QY 301 AlAspGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeu 320
DB 1139 GCTTCCCAAGAAATAATGATCATCTCTGTGAACACAGCAACACTGACAGGCTTCTT 1198
QY 321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnIlyIleLeuSer 340
DB 1199 TCTACCTTGGAGATATGCTGGATTCCTACCTGAGAAATAGATTAATATTCCTATCA 1258
QY 341 GluThrAspArgAspProLeuGlnValI 350
DB 1259 GAGACTGACAGAGGACCTCTCAGGTGATA 1288
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RESULT 2

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US-10-198-846-12938
; Sequence 12938, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12938
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1613..1614
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-12938
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Alignment Scores:

Pred. No.:	4,19e-194	Length:	1614
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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	54.57%	Indels:	0
DB:	14	Gaps:	0

US-09-745-506-37 (1-350) x US-10-198-846-12938 (1-1614)

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DB 679 GAGCGCCGTGGATGATCGGGCTCTGGAGAAAGCGGTATCTACTCTCATATCACACC 738
QY 103 TyrAspAlaAlaProIleGlnGlyValAsnAsnTrpLeuAlaIlySglYleuGlyAlaCysThr 122
DB 739 TATGATGTGGCGCCCGGCGGTCAACAACGTGTGCTTAAGGCTTGAGCTTGAC 798
QY 123 SerArgProIleHisProSerIlyAsnAlaProAsnYrProThrGluGlyAsnHisArgVal 142
DB 799 TCCAGGCCCATATCATCTTCCAAAGCTCCCAATACCTACAGAGGAAACCCAGGATA 858
QY 143 GluPheAsnValAsnYrThrGlnAspLeuAspYsValMetSerAlaValIlySglYle 162
DB 859 GAATTCACAGTTAACTATACACCAAGACCTGGCAAAAGTCATGTGAGTGAAGGAAT 918
QY 163 AspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGlnThrArgIle 182
DB 919 GACGGTGTTCGTCACTCTTTCTGCTAGACTGTAATGAGAGAACAAACAGGAT 978
QY 183 AsnLeuAsnCysThrGlnIlyAlaLeuMetGlnValIAspPheLeuSerArgAsnIys 202
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Db 979 AACGTGAATGTACTCAGAGCGCTTGATGATGTAGATTCTTCCCGAACA 1038
Qy 203 GlnLeuTyrGlnYthrGluIleLeuSerLeuGlnYlsProLeuLeuHsIstHly 222
Db 1039 CAACCTTATCTCAGAGCGGAAATCTGTCTACTGAGAGGCTTGTCTACATACGGA 1098
Qy 223 MetGlyArgLeuYsThrIleuAspGluSerValSerLeuAlaThrMetIleAspArgIle 242
Db 1099 ATGGAGCGTTATGACACACGTGATGATCTGTCTCCCTGGCACCATGATGATGATA 1158
Qy 243 LysArgHisLeuYlsLeuSerHisIleArgLeuAlaLeuGlnYlValGlyArgThrLeuGlu 262
Db 1159 AAAGACACCTAAACATCTCATATTCGCTTAGCCCTTGCGGTGGGAGCAACCTTAGAG 1218
Qy 263 SerGlnValYlsValAlaAlaLeuCysAlaGly 273
Db 1219 TCTCAAGTCAAAAGTCGTGCCCTGTGTGTGTGT 1251

RESULT 3

US-10-198-846-6276
; Sequence 6276, Application US/10198846
; Publication No. US2003009997A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steilmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6276
; LENGTH: 828
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6, 9, 16, 420, 498, 518, 520, 591, 630, 641, 643, 659, 661,
; LOCATION: 671, 674, 676, 679, 680, 681, 682, 683, 684, 685, 686, 687,
; LOCATION: 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699,
; LOCATION: 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722,
; LOCATION: 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734,
; LOCATION: 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746,
; LOCATION: 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769,
; LOCATION: 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781,
; LOCATION: 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793,
; LOCATION: 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816,
; LOCATION: 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-6276

Alignment Scores:
Pred. No.:
Score:

2.07e-86 Length: 828
90.00 Matches: 90

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 25.71%
DB: 14
Gaps: 0

US-09-745-506-37 (1-350) x US-10-198-846-6276 (1-828)

Qy 1 MetAspLeuYsAlaLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
Db 148 ATGATTTGAGGCTTCCCTTCTTCTTCTGATGATCTTTCATCTCTCTGCTGAG 207
Qy 21 SerTrpAsnValGlyLeuLeuValGluProSerProPheIstHrValAsnThrLeu 40
Db 208 AGTTGGACACATGTTGATTAAGTGTGGAACCAAGCCACACATAGCTAAATACACTC 267
Qy 41 PheLeuThrAsnAspLeuThrGluValMetGluValLeuGlnYlsYsAlaAsp 60
Db 268 TTCTGTACCAATGACCTGACTGAGGAGATGATGAGGAGGTGCTGCAAAAGACGAGAC 327
Qy 61 LeuIleLeuSerTyrHisProPheIlePheArgProMetLysArgIleThrTrpAsnThr 80
Db 328 CTCATTTCTCTTCAACATCCGCTATCTTCCGACCATGAAAGCCATTAACCTGGAACA 387
Qy 81 TrpYsGluArgLeuValIleArgAlaLeu 90
Db 388 TGGAAAGAGCGCCTGTGTATCCGGGCTCTG 417

RESULT 4

US-09-864-761-10530/c
; Sequence 10530, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21


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Db      1131 TTCTGTGACCAATGACCTGACGAGAGGATG 1099
RESULT 9
US-10-027-632-161386/C
; Sequence 161386, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161386
; LENGTH: 817
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-161386

Alignment Scores:
Pred. No.:      2.62e-07      Length:      817
Score:          16.00         Matches:      16
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    4.57%        Indels:      0
DB:             13           Gaps:        0

US-09-745-506-37 (1-350) x US-10-027-632-161386 (1-817)
Oy      265 VallysValAlaLeucyAlaGlySerGlySerValLeuGln 280
Db      69 GTCAAGTCGTGGCCCTGTGTCTGTGTGGAGCAGCTTCTGCAG 22

RESULT 10
US-10-027-632-161387/C
; Sequence 161387, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161387
; LENGTH: 817
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-161387

Alignment Scores:
Pred. No.:      2.62e-07      Length:      817
Score:          16.00         Matches:      16
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    4.57%        Indels:      0
DB:             13           Gaps:        0

US-09-745-506-37 (1-350) x US-10-027-632-161387 (1-817)
Oy      265 VallysValAlaLeucyAlaGlySerGlySerValLeuGln 280
Db      69 GTCAAGTCGTGGCCCTGTGTCTGTGTGGAGCAGCTTCTGCAG 22

RESULT 11
US-10-027-632-162668
; Sequence 162668, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162668
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-162668

Alignment Scores:
Pred. No.:      0.000396     Length:      765
Score:          13.00        Matches:      13
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    3.71%        Indels:      0
DB:             13           Gaps:        0

US-09-745-506-37 (1-350) x US-10-027-632-162668 (1-765)
Oy      9 SerLeuAsnAspPheAlaSerLeuSerPheAlaGlnSer 21
Db      345 TCCTTGAAATGACTTTCATCCCTCATTTCGTGAGAG 383

RESULT 12
US-08-781-986A-779/C
; Sequence 779, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 779:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; US-08-781-986A-779
;
; Alignment Scores:
; Pred. No.: 0.342 Length: 400
; Score: 10.00 Matches: 10
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 2.86% Indels: 0
; Gaps: 0
; DB:
;
; US-09-745-506-37 (1-350) x US-08-781-986A-779 (1-400)
;
; QY 19 AlagiusertTPASPasnValglyleu 28
; DB 212 GCTGAATCTTGGGATATGATGATGTTA 183
;
; RESULT 13
; US-08-781-986A-4577
; Sequence 4577, Application US/08/81986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 4577:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; US-08-781-986A-4577
;
; Alignment Scores:
; Pred. No.: 27.9 Length: 233
; Score: 8.00 Matches: 8
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 2.29% Indels: 0
; Gaps: 0
; DB:
;
; US-09-745-506-37 (1-350) x US-08-781-986A-4577 (1-233)
;
; QY 8 SerSerLeuSnsApphealaser 15
; DB 184 TCATCCTTAATGACTTTCAGACT 207
;
; RESULT 14
; US-09-764-869-65
; Sequence 65, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 383
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (363)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (372)
; OTHER INFORMATION: n equals a,t,g, or c
;
; US-09-764-869-65
;
; Alignment Scores:
; Pred. No.: 45 Length: 383
; Score: 8.00 Matches: 8
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 2.29% Indels: 0
; Gaps: 0
; DB:
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; US-09-745-506-37 (1-350) x US-09-764-869-65 (1-383)
;
; QY 3 LeuLySaLaLeuSerSerleu 10
; DB 65 CTGAAGGCCCTCTCTCTCTCG 88
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RESULT 15
US-10-091-504-65
; Sequence 65, Application US/10091504
; Publication No. US2003005908A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007C1
; CURRENT APPLICATION NUMBER: US/10/091,504
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ. ID NOS: 2442
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ. ID NO 65
; LENGTH: 383
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (363)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (372)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-091-504-65

Alignment Scores:
Pred. No.: 45 Length: 383
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.29% Indels: 0
DB: 14 Gaps: 0

US-09-745-506-37 (1-350) x US-10-091-504-65 (1-383)

QY 3 LeuYsAlaLeuLeuSerLeu 10
   |||||
Db 65 CTGAAGGCCCTCTCTCTCTG 88

Search completed: August 23, 2003, 23:06:33
Job time : 220 secs
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